

SEQUENCE LISTING

<110> Broze, George J., Jr.
<120> Protein Z-Dependent Protease Inhibitor
<130> WU-3110/1
<150> US 60/086,571
<151> 1998-05-19
<160> 16
<170> Word Perfect 5.0
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Leu Ala Pro Ser Pro Gln Ser Pro Glu Xaa Xaa Ala
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Arg Tyr Lys Gly Gly Ser Pro Xaa Ile Ser Gln Pro Xaa Leu
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 gtacatcatg ggcacacctaa c 21

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 Asn Leu Glu Leu Gly Leu Thr Gln Ser Phe Ala Phe Ile His Lys
 1 5 10 15

Asp Phe Asp Val

<210> 6
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 Met Ser Arg Ser Thr Gln Glu Leu Leu Gly Tyr His Cys Arg Leu
 1 5 10 15

Gln Asp Lys Leu Gln Glu Gln Glu Gly Ser Leu Ala Ala Glu Gly
 20 25 30

Arg His Ser Leu Ala Ser Ala Ala Asp His
 35 40

<210> 7
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 cagggatgtg tgctgtccca gggctgagaa gtggcaggtg agctggtgat 200
 tccttactgc ccaggttcgt tctaggaagg tgcgtcctca ccatgctgga 250

tgggtgccta gtccaggagc acccccctgag ctcctggcct agactccaaa	300
gggttgggta gatgagcaaa gactttacaa agaccttagg cgatatatgt	350
ccaggagcac ccaggaattt ctgggctacc actgcagact gcaggacaag	400
ctccaagaac aggaaggaag tcttgcagct gaagggaggc actccttggc	450
ctccgcagcc gat cac atg aag gtg gtg cca agt ctc ctg ctc Met Lys Val Val Pro Ser Leu Leu Leu -20 -15	493
tcc gtc ctc ctg gca cag gtg tgg ctg gta ccc ggc ttg gcc Ser Val Leu Leu Ala Lys Val Trp Leu Val Pro Gly Leu Ala -10 -5 -1 1	535
ccc agt cct cag tcg cca gag acc cca gcc cct cag aac cag Pro Ser Pro Gln Ser Pro Glu Thr Pro Ala Pro Gln Asn Gln 5 10 15	577
acc agc agg gta gtg cag gct ccc aag gag gaa gag gaa gat Thr Ser Arg Val Val Gln Ala Pro Lys Glu Glu Glu Glu Asp 20 25 30	619
gag cag gag gcc agc gag gag aag gcc agt gag gaa gag aaa Glu Gln Glu Ala Ser Glu Glu Lys Ala Ser Glu Glu Glu Lys 35 40	661
gcc tgg ctg atg gcc agc agg cag cag ctt gcc aag gag act Ala Trp Leu Met Ala Ser Arg Gln Gln Leu Lys Glu Thr 45 50 55	703
tca aac ttc gga ttc agc ctg ctg cga aag atc tcc atg agg Ser Asn Phe Gly Phe Ser Leu Leu Arg Lys Ile Ser Met Arg 60 65 70	745
cac gat ggc aac atg gtc ttc tct cca ttt ggc atg tcc ttg His Asp Gly Asn Met Val Phe Ser Pro Phe Gly Met Ser Leu 75 80 85	787
gcc atg aca ggc ttg atg ctg ggg gcc aca ggg ccg act gaa Ala Met Thr Gly Leu Met Leu Gly Ala Thr Gly Pro Thr Glu 90 95 100	829
acc cag atc aag aga ggg ctc cac ttg cag gcc ctg aag ccc Thr Gln Ile Lys Arg Gly Leu His Leu Gln Ala Leu Lys Pro 105 110	871
acc aag ccc ggg ctc ctg cct tcc ctc ttt aag gga ctc aga Thr Lys Pro Gly Leu Leu Pro Ser Leu Phe Lys Gly Leu Arg 115 120 125	913

gag acc ctc tcc cgc aac ctg gaa ctg ggc ctc aca cag ggg Glu Thr Leu Ser Arg Asn Leu Glu Leu Gly Leu Thr Gln Gly 130 135 140	955
agt ttt gcc ttc atc cac aag gat ttt gat gtc aaa gag act Ser Phe Ala Phe Ile His Lys Asp Phe Asp Val Lys Glu Thr 145 150 155	997
ttc ttc aat tta tcc aag agg tat ttt gat aca gag tgc gtg Phe Phe Asn Leu Ser Lys Arg Tyr Phe Asp Thr Glu Cys Val 160 165 170	1039
cct atg aat ttt cgc aat gcc tca cag gcc aaa agg ctc atg Pro Met Asn Phe Arg Asn Ala Ser Gln Ala Lys Arg Leu Met 175 180	1081
aat cat tac att aac aaa gag act cgg ggg aaa att ccc aaa Asn His Tyr Ile Asn Lys Glu Thr Arg Gly Lys Ile Pro Lys 185 190 195	1123
ctg ttt gat gag att aat cct gaa acc aaa tta att ctt gtg Leu Phe Asp Glu Ile Asn Pro Glu Thr Lys Leu Ile Leu Val 200 205 210	1165
gat tac atc ttg ttc aaa ggg aaa tgg ttg acc cca ttt gac Asp Tyr Ile Leu Phe Lys Gly Lys Trp Leu Thr Pro Phe Asp 215 220 225	1207
cct gtc ttc acc gaa gtc gac act ttc cac ctg gac aag tac Pro Val Phe Thr Glu Val Asp Thr Phe His Leu Asp Lys Tyr 230 235 240	1249
aag acc att aag gtg ccc atg atg tac ggt gca ggc aag ttt Lys Thr Ile Lys Val Pro Met Met Tyr Gly Ala Gly Lys Phe 245 250	1291
gcc tcc acc ttt gac aag aat ttt cgt tgt cat gtc ctc aaa Ala Ser Thr Phe Asp Lys Asn Phe Arg Cys His Val Leu Lys 255 260 265	1333
ctg ccc tac caa gga aat gcc acc atg ctg gtg gtc ctc atg Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val Val Leu Met 270 275 280	1375
gag aaa atg ggt gac cac ctc gcc ctt gaa gac tac ctg acc Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr Leu Thr 285 290 295	1417
aca gac ttg gtg gag aca tgg ctc aga aac atg aaa acc aga Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr Arg 300 305 310	1459

aac atg gaa gtt ttc ttt ccg aag ttc aag cta gat cag aag Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys 315 320	1501
tat gag atg cat gag ctg ctt agg cag atg gga atc aga aga Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg 325 330 335	1543
atc ttc tca ccc ttt gct gac ctt agt gaa ctc tca gct act Ile Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr 340 345 350	1585
gga aga aat ctc caa gta tcc agg gtt tta caa aga aca gtg Gly Arg Asn Leu Gln Val Ser Arg Val Leu Gln Arg Thr Val 355 360 365	1627
att gaa gtt gat gaa agg ggc act gag gca gtg gca gga atc Ile Glu Val Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile 370 375 380	1669
ttg tca gaa att act gct tat tcc atg cct cct gtc atc aaa Leu Ser Glu Ile Thr Ala Tyr Ser Met Pro Pro Val Ile Lys 385 390	1711
gtg gac cgg cca ttt cat ttc atg atc tat gaa gaa acc tct Val Asp Arg Pro Phe His Phe Met Ile Tyr Glu Glu Thr Ser 395 400 405	1753
gga atg ctt ctg ttt ctg ggc agg gtg gtg aat ccg act ctc Gly Met Leu Leu Phe Leu Gly Arg Val Val Asn Pro Thr Leu 410 415 420	1795
cta taa ttccaggacac gcataaggcac ttccgcgtgt aatgtatgc Leu 423	1841
aatctgaggt atcaaacaca cacaggatac cagcaatgga tggcagggga gagtgttcct tttgttctta actagtttag ggtgttctca aataaataca gtagtcggca cttatctgag gggatacat tcaaagaccc ccagcagatg cctgaaacgg tggacagtgc tgaaccttat atatatttt tcctacacat acatacctat gataaaagttt aatttataaa ttaggcacag taagagatata acaataataa caacattaag taaaatgagt tacttgaatg caagcactgc aataccataa cagtcaaact gattatagag aaggctacta agtgactcat gggcgaggag catagacagt gtggagacat tggcaaggg gagaattcac atcctgggtg ggacagagca ggacaatgca agattccatc ccactactca	1891 1941 1991 2041 2091 2141 2191 2241 2291

gaatggcatg ctgcttaaga cttttagatt gtttatttct ggaattttc 2341
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 atattttta aaaaaaaaaa aaaaa 2466

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 Met Lys Val Val Pro Ser Leu Leu Leu Ser Val Leu Leu Ala
 -20 -15 -10

Lys Val Trp Leu Val Pro Gly Leu Ala Pro Ser Pro Gln Ser
 -5 -1 1 5

Pro Glu Thr Pro Ala Pro Gln Asn Gln Thr Ser Arg Val Val
 10 15 20

Gln Ala Pro Lys Glu Glu Glu Asp Glu Gln Glu Ala Ser
 25 30 35

Glu Glu Lys Ala Ser Glu Glu Glu Lys Ala Trp Leu Met Ala
 40 45

Ser Arg Gln Gln Leu Ala Lys Glu Thr Ser Asn Phe Gly Phe
 50 55 60

Ser Leu Leu Arg Lys Ile Ser Met Arg His Asp Gly Asn Met
 65 70 75

Val Phe Ser Pro Phe Gly Met Ser Leu Ala Met Thr Gly Leu
 80 85 90

Met Leu Gly Ala Thr Gly Pro Thr Glu Thr Gln Ile Lys Arg
 95 100 105

Gly Leu His Leu Gln Ala Leu Lys Pro Thr Lys Pro Gly Leu
 110 115

Leu Pro Ser Leu Phe Lys Gly Leu Arg Glu Thr Leu Ser Arg
 120 125 130

Asn Leu Glu Leu Gly Leu Thr Gln Gly Ser Phe Ala Phe Ile
 135 140 145

His Lys Asp Phe Asp Val Lys Glu Thr Phe Phe Asn Leu Ser
 150 155 160

Lys Arg Tyr Phe Asp Thr Glu Cys Val Pro Met Asn Phe Arg
165 170 175

Asn Ala Ser Gln Ala Lys Arg Leu Met Asn His Tyr Ile Asn
180 185

Lys Glu Thr Arg Gly Lys Ile Pro Lys Leu Phe Asp Glu Ile
190 195 200

Asn Phe Glu Thr Lys Leu Ile Leu Val Asp Tyr Ile Leu Phe
205 210 215

Lys Gly Lys Trp Leu Thr Pro Phe Asp Pro Val Phe Thr Glu
220 225 230

Val Asp Thr Phe His Leu Asp Lys Tyr Lys Thr Ile Lys Val
235 240 245

Pro Met Met Tyr Gly Ala Gly Lys Phe Ala Ser Thr Phe Asp
250 255

Lys Asn Phe Arg Cys His Val Leu Lys Leu Pro Tyr Gln Gly
260 265 270

Asn Ala Thr Met Leu Val Val Leu Met Glu Lys Met Gly Asp
275 280 285

His Leu Ala Leu Glu Asp Tyr Leu Thr Thr Asp Leu Val Glu
290 295 300

Thr Trp Leu Arg Asn Met Lys Thr Arg Asn Met Glu Val Phe
305 310 315

Phe Pro Lys Phe Lys Leu Asp Gln Lys Tyr Glu Met His Glu
320 325

Leu Leu Arg Gln Met Gly Ile Arg Arg Ile Phe Ser Pro Phe
330 335 340

Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg Asn Leu Gln
345 350 355

Val Ser Arg Val Leu Gln Arg Thr Val Ile Glu Val Asp Glu
360 365 370

Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile Thr
375 380 385

Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe
390 395

His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe
400 405 410

Leu Gly Arg Val Val Asn Pro Thr Leu Leu
415 420

<210> 9
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Glu Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile Thr
1 5 10 15

Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe His
20 25 30

Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe Leu Gly
35 40 45

Arg Val Val Asn Pro Thr Leu Leu
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<210> 10
<211> 53
<212> PRT
<213> Artificial Sequence

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<400> 10

Glu Arg Gly Thr Glu Val Val Ser Gly Thr Val Ser Glu Ile Thr
1 5 10 15

Ala Tyr Cys Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe His
20 25 30

Phe Ile Ile Tyr Glu Glu Met Ser Arg Met Leu Leu Phe Leu Gly
35 40 45

Arg Val Val Asn Pro Thr Val Leu
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<210> 11
<211> 53
<212> PRT
<213> Artificial Sequence

<220>

<400> 11

Glu Lys Gly Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile
1 5 10 15

Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val
20 25 30

Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly
35 40 45

Lys Val Val Asn Pro Thr Gln Lys
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<210> 12

<211> 53

<212> PRT

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<400> 12

Glu Lys Gly Thr Glu Ala Thr Gly Ala Pro His Leu Glu Glu Lys
1 5 10 15

Ala Trp Ser Lys Tyr Gln Thr Val Met Phe Asn Arg Pro Phe Leu
20 25 30

Val Ile Ile Lys Glu Tyr Ile Thr Asn Phe Pro Leu Phe Ile Gly
35 40 45

Lys Val Val Asn Pro Thr Gln Lys
50

<210> 13

<211> 56

<212> PRT

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<400> 13

Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala
1 5 10 15

Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe Lys Ala Asn Arg
20 25 30

Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn Thr Ile Ile
35 40 45

Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
50 55

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<211> 53

<212> PRT

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Glu Glu Gly Thr Gln Ala Thr Thr Val Thr Thr Val Gly Phe Met
1 5 10 15
Pro Leu Ser Thr Gln Val Arg Phe Thr Val Asp Arg Pro Phe Leu
20 25 30
Phe Leu Ile Tyr Glu His Arg Thr Ser Cys Leu Leu Phe Met Gly
35 40 45
Arg Val Ala Asn Pro Ser Arg Ser
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<211> 50
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Glu Asp Gly Thr Lys Ala Ser Ala Ala Thr Thr Ala Ile Leu Ile
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Ala Arg Ser Ser Pro Pro Trp Phe Ile Val Asp Arg Pro Phe Leu
20 25 30
Phe Phe Ile Arg His Asn Pro Thr Gly Ala Val Leu Phe Met Gly
35 40 45
Gln Ile Asn Lys Pro
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<210> 16
<211> 12
<212> PRT
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